



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

*In re* Application of ) Group Art Unit: 1645  
ZHELNIN and BLOOMQUIST ) Examiner: S. Gucker  
Serial No. 09/899,532 )  
Filing Date: July 6, 2001 ) Docket No. 02973.00040

For: **HUMAN NEUROPEPTIDE Y-LIKE G PROTEIN-COUPLED RECEPTOR**

**SUBMISSION OF SUBSTITUTE DECLARATION UNDER 37 C.F.R. § 1.131**

U.S. Patent and Trademark Office  
220 20th Street S.  
Customer Window, Mail Stop Amendment  
Crystal Plaza Two, Lobby, Room 1B03  
Arlington, VA 22202

Dear Sir:

Applicants responded on June 25, 2004 to the Office Action mailed February 25, 2004 in the application referenced above. The response included a declaration of the inventors under 37 C.F.R. § 1.131, which included Exhibits 1-10. The declaration stated that the dates on Exhibits 1-10 had been redacted; however, the Exhibits 1-10 filed together with the declaration inadvertently contained dates.

A substitute declaration with Exhibits 1-10 accompanies this paper. The declaration itself is a copy of the one filed June 25, 2004. Exhibits 1-10 are identical to those filed June 25, 2004 except that the dates have been redacted.

Please substitute the declaration and exhibits that accompany this paper for those filed June 25, 2004. Please discard the declaration and exhibits filed June 25, 2004 and delete all copies of the declaration and exhibits that may have been scanned electronically.

We believe no fee is associated with this request. If a fee is required, please charge our Deposit Account No. 19-0733.

Respectfully submitted,  
BANNER & WITCOFF, LTD.

Date: July 6, 2004

By:

Lisa M. Hemmendinger  
Lisa M. Hemmendinger  
Registration No. 42,653

Customer No. 22907



PATENT

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

*In re Application of:*

ZHELNNIN and BLOOMQUIST

) Group Art Unit: 1645

Serial No. 09/899,532

) Examiner: S. Gucker

Filing Date: July 6, 2001

) Docket No. 02973.00040

For: HUMAN NEUROPEPTIDE Y-LIKE G PROTEIN-COUPLED RECEPTOR

DECLARATION UNDER 37 C.F.R. § 1.131

U.S. Patent and Trademark Office  
220 20th Street S.  
Customer Window, Mail Stop Non-Fee Amendment  
Crystal Plaza Two, Lobby, Room 1B03  
Arlington, VA 22202

Dear Sir:

We, Leonid Zhelnin and Brian Bloomquist, declare as follows:

1. We are the named inventors of the subject matter claimed in the application referenced above.
2. Prior to March 2, 2000, we reduced to practice the subject matter of claims 1-8 and 12 of the application referenced above. The dates on the attached exhibits have been redacted; however, all the work described in this declaration was performed in the United States prior to March 2, 2000.
3. Prior to March 2, 2000, we monitored search results from a program (Gene Agent) that automatically checked sequences released into the public domain for homology to the orexin and NPY1 receptors. Prior to March 2, 2000, we received reports from the orexin-

and NPY1-receptor Gene Agent searches, respectively, indicating that DNAs with accession numbers EM:AC005961 (Homo sapiens Chromosome 11q12.2 PAC pDJ32L16 genomic DNA) and GB:g3823006 (Human sperm genomic library) both had homology to the orexin and NPY1 receptor sequences. Copies of the reports are attached as Exhibit 1. Sequence analysis revealed these DNAs to be overlapping and that AC00596 contained 154,647 nucleotides comprising what appeared to be at least five exons with homology to the orexin receptor. A copy of BLAST comparisons of the translated five exons with the amino acid sequence of the orexin receptor is attached as Exhibit 2.

4. Prior to March 2, 2000, we used sequence information from AC00596 to amplify by polymerase chain reaction (PCR) amplification two PCR products of 234 and 111 bp from genomic DNA. The longer 234 bp clone included both transmembrane domains (TM 1 and 2 of the putative GPCR. A copy of the nucleotide sequence of the PCR product is attached as Exhibit 3.

5. We designed primers to the 5'- and 3'-regions of the 234 bp clone, and 5'- and 3'-RACE amplifications were carried out to clone the full coding region of the putative GPCR. The reverse primers used in the strategy were termed "6A1-85B" and "6A1-126B" and are shown on pages 2 and 3 of Leonid Zhelnin's laboratory notebook no. RB53651. Copies are provided as Exhibit 4.

6. Prior to March 2, 2000, we obtained two 5'-RACE clones (~220 and ~320 bp) from human heart cDNA; sequence analysis of the 5'-RACE clone 5GA1 revealed that it encodes a peptide with homology to the N-terminal 105 amino acids of NPY1. A copy of page 47 of Leonid Zhelnin's laboratory notebook no. RB53651 showing a ClustalW-formatted alignment of the amino acid sequence encoded by 5GA1 and the amino acid sequence of the neuropeptide Y-1

receptor (NPY-1R.pep) is provided as Exhibit 5. The position of the putative START methionine codon (ATG) in clone 5GA1 was consistent with clone 5GA1 being similar to the NPY-1 and orexin-2 receptors. The identity of this ATG as the true START codon was unconfirmed, however, because the open reading frame (ORF) was not closed upstream of the 5'-most ATG.

7. Sequence analysis of the 3'-RACE amplicon (~0.9 kb in length; 3'-RACE #2 clone) revealed that this clone contained sequences homologous to a GPCR through TM6. The primers used in the 3'-RACE strategy were termed "6A1-F32" and "6A1-F41" and are shown on pages 4 and 5 of Leonid Zhelnin's laboratory notebook no. RB53651. Copies are provided as Exhibit 6. However, the 3'-RACE amplicon lacked both a TM7 domain and corresponding STOP codon. A complete clone was electronically assembled from the 3'-RACE amplicon and clone 5GA1 to create a 1047-bp sequence contig, which encoded 349 amino acids and which was named GA1. A copy of page 53 of Leonid Zhelnin's laboratory notebook no. RB5361 showing the electronically assembled sequence is provided as Exhibit 7.

8. Prior to March 2, 2000, GA1 was used as template to search the Image Consortium database for novel expressed sequence tags (ESTs, which are cDNAs) with identity to GA1 to identify the missing 3'-end. Three Image clones from human kidney were identified and found to have similarity based on our previous sequence analysis. Identification of the three Image clones was recorded on page 61 of Leonid Zhelnin's laboratory notebook no. RB53651; a copy is provided as Exhibit 8.

9. Sequence analysis of Image clone 2055185 confirmed the putative START methionine because sequence analysis revealed it to contain an in-frame STOP codon upstream

of the putative START methionine. This sequence information is summarized on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651; a copy is provided as Exhibit 9.

10. Under our direction the 3'-ends of the Image cDNAs (from the NCI\_CGAP\_Kid12 and Soares NFL\_T\_GBC\_S1 libraries) were sequenced. One of the Image clones had an extended 3'-end that included the presence of a 710-bp intron followed by what appeared to be further exonic sequence.

11. The sequence immediately downstream of the intron of this Image cDNA clone was used as the query to search (via the BLAST algorithm) the genomic sequence within AC005961 to identify the missing 3'-coding region. Prior to March 2, 2000, BLAST analysis identified the missing 271 nucleotides of the 3'-end of the coding region of the GCR. This sequence information is summarized on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651. See Exhibit 9.

12. Prior to March 2, 2000, we amplified clones containing the complete 1293-bp ORF from both human heart and brain cDNA by PCR (using Marathon-Ready cDNA libraries, Clontech) and recorded this information on page 89 of Leonid Zhelnin's laboratory notebook no. RB53651. See Exhibit 9.

13. Also prior to March 2, 2000, the coding sequence of the full-length cDNA clone was confirmed by sequence analysis of a full-length amplicon generated by PCR from human brain cDNA. This sequence was recorded on pages 95-97 of Leonid Zhelnin's laboratory notebook no. RB53651; copies of these pages are provided as Exhibit 10. The coding sequence is contained within SEQ ID NO:1 of our provisional application Serial No. 60/215,523 and within SEQ ID NO:1 of our utility application 09/899,532. This coding sequence encodes the 431 amino acid sequence shown in SEQ ID NO:2 of both the provisional and utility applications.

14. All statements made herein of our own knowledge are true and all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issuing thereon.

Dated: June 25, 2004

Brian T. Bloomquist

Brian Bloomquist, Ph.D.

Dated: June 25, 2004

Leonid Zhelnin

Leonid Zhelnin, Ph.D.



## Analysis Results

Home	Logout	Seq Analysis	Utilities	Grid/Excel	Help
Project ID: <b>oxrin</b>	Project Name: oxrin receptor homology search	Created: Zhalnin, Leonid	Modified: It_Account, Admin	Status: Current User: Zhalnin, Leonid (WRITE)	Today's Date: Num Seqs: 7

Analysis Data

These results are saved. Use the buttons to change the state of these results.

Save these results  Discard these results

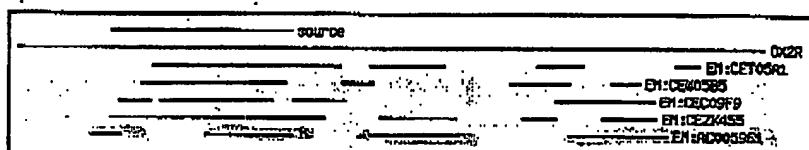
Description:

## Maximum Number of Hits per Hit Class

Trans. Protein:   
 Feature roll-up:  Off  On  
 Redisplay

## View parameters

## Protein Agent



oxrin:OX2R:1

Hit ID	P-Value	% Ident.	Description				Hit Class
<input checked="" type="checkbox"/> EM:CEW0581:5 Result Details	2.5e-17	40	Caenorhabditis elegans cosmid T05A1				Trans. Protein
	Feature		Description				Feature Metric
	source		Left End	Right End	Strand	Component Description	Component Metric
<input checked="" type="checkbox"/> EM:CEW0585:5 Result Details	4.7e-17	33	Caenorhabditis elegans cosmid W05B5				Trans. Protein
	Feature		Description				Feature Metric
	source		Left End	Right End	Strand	Component Description	Component Metric
<input checked="" type="checkbox"/> EM:CEW0599:5 Result Details	7.4e-17	35	Caenorhabditis elegans cosmid C09F9				Trans. Protein
	Feature		Description				Feature Metric
	source		Left End	Right End	Strand	Component Description	Component Metric

EM:CEC0999:5 Result Details		source	Component Description				Component Metric		
Hit ID	P-Value	% ident.	Description						
	9.3e-14	26	Caenorhabditis elegans cosmid ZX455						
EM:CEBxx455:5 Result Details		Feature	Description				Feature Metric		
		source							
Hit ID	P-Value	% ident.	Left End	Right End	Strand	Component Description	Component Metric		
	1.8e-12	32	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PNC pDJ32L16; HTG6 phase 1, 8 unordered pieces.						
EM:ACDD5961:1 Result Details		Feature	Description				Feature Metric		
		source							
Hit ID	P-Value	% ident.	Left End	Right End	Strand	Component Description	Component Metric		

Select All  Deselect All

Save to Project  Submit  Reset

Requested by: Zhelnin, Leonid on

 INCYTE PHARMACEUTICALS, INC.

File	Menu	Project	Output	Seq. Analysis	Utilities	Gene Agent	Help
Project ID:	orexin	Project Name:	orexin receptor homology search				
Created:		Created By:	Zhelnin, Leonid				
Modified:		Modified By:	lt_Account, Admin				
Status:		Current User:	zhelnin, Leonid (WRITE)				
Today's Date:		Num Seqs:	7				

Project Manager	Project Status

Sequences (7 of 7 shown, 7 Active):					
Sequence ID	Type	Parent	Created By	Created	Status
<a href="#">orexin:q3823006:1</a>	DNA	<a href="#">GB:q3823006</a>	Zhelnin, L.		OPEN
HS_2052_B1_G04_T7	CIT Approved Human Genomic Sperm Library	D	Homo sapiens genomic	lone	
Plate=2052	Col=7	Row=N,	genomic survey sequence.		
<a href="#">orexin:AC005961:1</a>	DNA	<a href="#">EM:AC005961</a>	Zhelnin, L.		OPEN
*** SEQUENCING IN PROGRESS ***	Homo sapiens Chromosome 11q12.2	PAC pDJ32L16; HTGS	base 1, 8		
unordered pieces.					
<a href="#">orexin:frame1_AC005961:1</a>	PRT		Zhelnin, L.		OPEN
<a href="#">orexin:neworexin.pep:1</a>	PRT		Zhelnin, L.		OPEN
<a href="#">orexin:G2897124:1</a>	PRT	<a href="#">ST:G2897124</a>	Zhelnin, L.		OPEN
OREXIN RECEPTOR-1.					
<a href="#">orexin:OX2R:1</a>	PRT		Zhelnin, L.		OPEN
P1;G2897128 - orexin receptor-2 - Homo sapiens (human)					
<a href="#">orexin:AP041243:1</a>	RNA	<a href="#">EM:AP041243</a>	Zhelnin, L.		OPEN
Homo sapiens orexin receptor-1 mRNA, complete cds.					

Manage Sequences	Search Sequences

Gene Agent Results (10 of 166 shown, 166 active):						
Agent Name	Results	Started On	Description	Status	Method	Job Status
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed
<a href="#">NEWOREXIN</a>	+			SAVED	Protein Agent	Completed

View All Gene Agent Results

No Project Annotation

View All Annotations	View All Taxon Annotations

Requested by: Zhelnin, Leonid

## LifeTools

## Query Detail

Main Menu	Projects	Entries	Sequence Analysis	Utilities	Login/Logout	Help
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Sequence: orexin:AC005961:1 [Add Sequence Annotation](#)

Entries with the same Physical Sequence

[EM:AC005961](#)

[GB:g3859648](#)

[Imagelga:g3859648:1](#)

[Newgage:AC005961:1](#)

[FASTA](#)

General Information About The Entry

Sequence ID	AC005961
Version	1
Sequence Description	*** SEQUENCING IN PROGRESS *** Homo sapiens Chromosome 11q12.2 PAC pDJ32L16; HTGS phase , 8 unordered pieces.
Project	orexin
Project Name	orexin receptor homology search
Molecule	DNA
Sequence Information	
Length	154647

 INCYTE PHARMACEUTICALS, INC.

Sequences producing High-scoring Segment Pairs:	Smal		
	Reading Frame	High Score	Proba P(N)
AC005961 *** SEQUENCING IN PROGRESS *** Homo sapien..	+2	103	1.8e-
Score = 103 (48.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 17/52 (32%), Positives = 33/52 (63%), Frame = (+2)			
Query: 112 LVVDITETWFFGQSLCKV1PYLQTVSVSVLILSCIALDRWYAIChPLMK 163 L+ D++ G +CK++P++Q+ +V +LT++CIA++R + HP K Sbjct: 48452 LMYDLSYFLTAGAFICKMVFFVQSTAVVTEILIMTCIAVERHQGLVHPFKMK 48607			
Score = 88 (41.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 15/54 (27%), Positives = 31/54 (57%), Frame = (+3)			
Query: 210 CDERWGGEIYPKMYHICFFLVTVMAFLCLMVLAYLQIFRKLCRQIPGTSSVQ 263 C B W ++ K+Y ++ ++ PL +M++ Y +I +LW ++ G SV++ Sbjct: 56082 CLEEWWTSPVHQKIYTTFILVILFLLPLMVMLILYSKIGYELWIKKRVDGSEVLR 56243			
Score = 71 (33.3 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 15/54 (27%), Positives = 26/54 (48%), Frame = (+1)			
Query: 329 VFGMFAHTEDETVYAWFTFSHWLVYANSAANPIIYNFLSGKTFREEFKAAFSCC 382 + G F D T+ F + ++NS NPI+Y F++ F++ +A C Sbjct: 59380 ISGNFEKEYDDVTIKMIFAIVQIIGFSNSICNPIIVYAFMNENFKKNVLSAVCYC 59541			
Score = 47 (22.1 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 9/17 (52%), Positives = 11/17 (64%), Frame = (+2)			
Query: 46 EYLHPKEYEWVLIAGYI 62 EY H +E W LI+ YI Sbjct: 29786 EYPHAEENWTLISQYI 29836			
Score = 46 (21.6 bits), Expect = 1.8e-12, Sum P(5) = 1.8e-12 Identities = 6/8 (75%), Positives = 7/8 (87%), Frame = (+3)			
Query: 381 CCCLGVHH 388 CCCLG+ H Sbjct: 148296 CCCLGLEH 148319			



## Retrieve FASTA Sequences

[Main Page](#) [Projects](#) [Open](#) [Seq Analysis](#) [Utilities](#) [Login / Logout](#) [Help](#)

Project ID: Newgage Project Name: Cloning new gene agent search sequences  
Created: Created By: Zhein, Leonid  
Modified: Modified By: Zhein, Leonid  
Status: OPEN Current User: Zhein, Leonid (WRITE)  
Today's Date: Num Seqs: 30

>Newgage:GA2:1 per product of ac acI primers of AC00596 genomic chromosome se  
GTATGATTATCCTATTCCCTACTGCAGGTGCCTTCATTTGCAAGATGGTGCCATTGTCAGTCTACCGCTGTTGTGA  
CAGAAATCCTCACTATGACCTGCATTGCTGTEGAAAGGCACCCAGGGACTTGTGCATCCTTTAAATGAAGTGGCAATAC  
ACCAACCGAAGGGCTTCACAATGCTAGGTGAGGCCACTGGATGTGCCAATGGCAGTGTGAATGACATTCTCA

Requested by: Zhein, Leonid on

 INCYTE PHARMACEUTICALS, INC.

## **BAYER CORPORATION**

47

**SUBJECT**

**6A1-5 RACE Project**

Fig. 8.3 A. Städtegr. 1:1 MM

### Unified Sequence A, B, C

總計數額 15,188

## 5GA1 Aligned Sequences Formatted Alignment

## ClustalW Formatted Alignments

**SGA1** 10 20 30  
**NPY-1R.pep** M Q A L N I T P E Q F S R L L L R D H N L T R E F I L Y R  
M N S T L F S Q V E N H S V H S N F S E K N A L L F E N

5GA1 NPY-1R.pep      LRPLVYTP[E]GRAKLA[AI]V[E]GVLIF[A]AL  
 40 50 60  
 D - - - D C H [E] L A M I F T D A [A] Y G A V I I G V

**5GA1** F E G A L V F Y V V T R S A A V T F C S I A L S G A I  
**NPY-1R.pep** S G I L A L I I I I L K Q R E N A N N L V N T S P

5GA1 NPY-1R.pep 100 I E T F F I P V M K P 110 120  


**SIGNED BY**

DATE

**WITNESSED AND UNDERSTOOD BY**

DATA

4

## BAYER CORPORATION

SUBJECT

3' RACE

1

2

3 Translated Sequence

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5 Range: 1 to 161

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641 F 41

New

Page 1

10 20 30 40 50  
 AGTGTACTCATGCCCTGGCGCTTTGGAAATGGCTGGTGTCTACGTCACATGAGTAGCGGGACCGCGAGAAACCGTTACCGAGACCAAGATGCA  
 S V L I A L A L F G N A L V F Y V >  
 TRANSLATION OF GAI.TXT [A] →

60 70 80 90 100  
 → Nested 641  
 CCACTGGCGCTCGTCCGGTACCGTGGCAGTGGTTGAGAAATACACCA  
 V T R S K A M R T V T N I F I C >  
 TRANSLATION OF GAI.TXT [A] →

110 120 130 140 150  
 CTTGGCGCTCAGTGACCTGCTCATCACCTCTCTGCATTCCCGTCACC  
 GGAACCGCGAGTCACTGGACGAGTAGTGGAAAGAAGACCTAAGGCCACTGG  
 S L A L S D L L - T P F C I P V T >  
 TRANSLATION OF GAI.TXT [A] →

150  
 ATGAAAGCCGAA  
 TACTTCGGCTT  
 M K P X >

to order  
 for labeling

3' race

41 22 188 167 53.9 78.0 3.5 56.7 60.4 56.8 48.1 48.1 -3.6 -8.3  
 CTCCTGCGATTCGCTTCAC 27 -43.6 -199.5 -515.1 CTCCTGCGATTCGCTTCAC 27 -43.0 -205.0 -536.4

12 74 188 115 52.2 55.4 1.1 54.9 58.6 56.0 40.0 40.1 4.4 -8.3

CTCTGCGATTCGCTTCAC 25 -9.2 -102.9 -471.0

SIGNED BY

Spree

DATE

WITNESSED AND UNDERSTOOD BY

Zee Zee

DATE

CROSS REFERENCES:

## BAYER CORPORATION

## Touch Down PCR for GAT RACE

15	5 $\mu$ l cDNA template (Heart) (Brain)	1
16	36 $\mu$ l H <sub>2</sub> O	2
17	5 $\mu$ l 10x cDNA Buffer	3
18	1 $\mu$ l dNTP Mix (0.4M)	4
19	1 $\mu$ l Ado cDNA polymer mix (50X)	5

43  $\mu$ l Final + 3  $\mu$ l AP1

program 1 (preferred: use if GSP T<sub>m</sub> > 70°C):

PE DNA Thru

Heart	1	B126	{ }
	2	F32	
	3	F41	
Brain	4	B126	{ }
	5	F32	
	6	F41	

PE GeneAmp Systems 2400/9600  
(or hot-lid thermal cycler):

- 94°C for 30 sec
- 5 cycles:
  - 94°C 5 sec
  - 72°C 4 min<sup>0</sup>
- 5 cycles:
  - 94°C 5 sec
  - 70°C 4 min<sup>0</sup>
- 20-25 cycles:
  - 94°C 5 sec
  - 68°C 4 min<sup>0</sup>

PRODUCT: Human Heart  
Marathon-Ready™ cDNA

CATALOG #: 7404-1

## DESCRIPTION:

Marathon-Ready cDNA is high-quality, double-stranded cDNA which has been ligated to the Marathon™ Adaptor and is ready for use as a template in 5' and 3' Marathon RACE reactions. In many cases, the full-length cDNA can then be obtained by end-to-end amplification or standard cloning. Enough material is provided for 30 50- $\mu$ l Marathon RACE reactions.

LOT #: 9010719

CONCENTRATION: = 0.1 ng/ $\mu$ l

## STORAGE BUFFER:

- 10 mM Tricine-KOH (pH 9.2)
- 1 mM EDTA

POLY A<sup>+</sup> RNA SOURCE:

Normal, whole hearts pooled from 3 male Caucasians, ages 28-47; cause of death: trauma

## STORAGE CONDITIONS:

- -20°C
- Avoid multiple freeze/thaw cycles.

No further RNA source information is available.

SIGNED BY

WITNESSED AND UNDERSTOOD BY

CROSS REFERENCES:

DATE

Page

## **BAYER CORPORATION**

53

**SUBJECT**

huma<sup>6A1</sup> project. Full length 5' + 3' ends.

1 New sequence was deposited in the Life Tools  
of unknown protein and called 6A. pep. 4

W<sub>1</sub> 1 - Forward

chart

37-26254 (9.27)  
Sauvignon '31 1651

349 AA

1047 t.p. Lang

5' GTR conservative 104+ 8  
5' GTR conservative 9  
5' GTR conservative 10  
5' GTR conservative 11  
5' GTR conservative 12  
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5' GTR conservative 31  
5' GTR conservative 32  
5' GTR conservative 33  
5' GTR conservative 34

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## CROSS REFERENCES

DATE

DATE

**BAYER CORPORATION**

61

SUBJECT

Image clones matching 6A1

1m	2055532	g4001837	1
1m	2055185	g4002759	2
1m	2091776	g4187861	3
			4
			5
			6
			7

## DNA vs EST Homology Search

source	g400183
GB:g400	337
GB:g400	759
GB:g4187861	

g4001837

Hit ID #	P-Value	% ident.	Description
<u>GB:g4001837</u> (Detail)	0	100	tb27a03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA
Feature	Start	Stop	Description
source	1	432	

analysis Results: 28499

[http://lifetools-e.wh.bayer.com/cgi-bin/Incyte/LifeTools/2.0/LT\\_viewer?id=28499](http://lifetools-e.wh.bayer.com/cgi-bin/Incyte/LifeTools/2.0/LT_viewer?id=28499)

Hit ID #	P-Value	% ident.	Description	AM
<u>GB:g4002759</u> (Detail)	0	100	tb23d09.x1 NCI_CGAP_Kid12 Homo sapiens cDNA	
Feature	Start	Stop	Description	
source	1	432		

Hit ID #	P-Value	% ident.	Description	AM
<u>GB:g4187861</u> (Detail)	6.2e-43	100	te67e05.x1 Soares_NFL_T_GBC_S1 Homo sapiens	
Feature	Start	Stop	Description	
source	3	127		

Acc. Num.	Image/Unigene	Insert	Read		
	TIGR Indices	Length	Length	HQSS	Source (Age/Sex)
AI307658	Im:2055532 Hs.181638	1414	432	419	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))
AI308124	Im:2055185 Hs.181638	1308	432	429	NCI_CGAP_Kid12 library made from kidney (2 pooled tumors (clear cell type))
AI378908	Im:2091776 Hs.181638	404	364	364	Soares_NFL_T_GBC_S1 library made from pooled

SIGNED BY

DATE

WITNESSED AND UNDERSTOOD BY

DATE

CROSS REFERENCES



95

## BAYER CORPORATION

SUBJECT

Sequencing results of L621/pT7Blue

1 1. Check if L. Taylor going to close P.E. register.  
2  
3  
4

5 1). Clone #1 sop is ok with one polymorphic  
6  
7

8 \*\*\* DNA Striderver 1.2 \*\*\*

9 L621/pT7Blue#1 sop -> Graphic Map

10 DNA sequence 1587 b.p. caatgttcgtatc ... ccgttcgtttttt linear

11 432 AA

12 14 165 Exons/105 Introns

38	SmaI	1576 SacI
20	XbaI	1573 Gcl II
23	PstI	1573 EcoI
20	SstI	1559 SacI
20	HincII	1559 Eco136I
13	Sse8397I	1559 BamI
21	297 FspI	1553 KpnI
8	HpaII	1553 Acc65I
8	SphI	1544 BamHI
8	NspC1	1521 BsgI
8	Nsp7524I	1465 AII
8	220 SgrA1	1395 Eco57I
8	277 BstEII	619
2	HindIII	
19	164 BstEII	
2	227 BstEII	
2	200 BglI	
2	450 NspBII	
2	695 AciI	
2	705 BglII	
2	814 PmlI	
2	826 BstBII	
2	768 Bsp1407I	
2	1065 Pau101	
2	1085 NsiI	
2	1521 BsgI	

21 70 ATG 1587 base pairs Unique Sites 1366 STOP

22

23 2) Clone #17 K. Brain is good (same orientation)  
24 with tt -> ttc (Phe) 917 AA

25  
26 3) Clone #16 K. Heart is good  
27 with atc -> Att (Ile) 216 AA

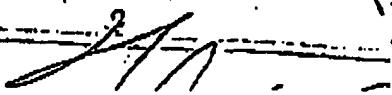
28 ↓ cloned using TA-cloning  
29 by penta 3 10 kbp's.

30 XbaI/Bam 3.1(-)

31 KpnI (1)

32 KpnI (1)

33 SIGNED BY

34 

# **BAYER CORPORATION**

**SUBJECT**

Full length cDNA of L6Z1 (npy-like)

in  $\rho C \bar{\sigma} N A = 3 = 1 = T \bar{\sigma} \mu \bar{\sigma}$

#1scop/pCDNA3.1Topo  
Sequencher™ "Untitled Project"

HindIII (6)  
KpnI (16)  
SacI (22)  
SamHI (24)  
SpeI (30)  
BstXI (43)  
SmaI (61)

PstI (1560)  
EcoRV (1563)  
BstXI (1573)  
NotI (1578)  
XmaIII (1578)  
XbaI (1584)  
XbaI (1590)  
DraII (1596)  
ApaI (1600)  
SacII (1603)

PstI (1113) EcoRI (1344)

SacII (1603)

Mapping all cutsites.  
Cutters : ApaI, BamHI, BstXI, DraI, EcoRI, EcoRV, HindIII, KpnI, NotI, PstI, SacI, SacII, SmaI, SphI, XbaI, XbaII & XbaIII  
Non-Cutters : Bsp106 & Sall

### Mapping all cutsites

Chant

Digitized by srujanika@gmail.com

WITNESSED AND UNDERSTOOD BY

#### **CROSS REFERENCES.**

## **BAYER CORPORATION**

97

**SUBJECT**

1155785  
1356970  
1587928

Bacterioph.  
contaminated?

1  
2  
3  
4

## BAYER CORPORATION

SUBJECT

5' RACE 641

1 9 1 85 15 51.1 74.1 4.9 54.1 56.8 61.7 48.1 60.0 3.3 1.1  
 2 1 CCGCTTAAAGGACTCTTCTTACGCC 27 -13.1 -205.0 -536.1 GGTGTTAGCTGAGCTACAGAC 25 -41.9 -184.5 -470.9 641-S  
 3 1 IV 1 126 126 51.8 77.0 1.7 56.0 56.8 59.6 48.1 49.0 4.3 -7.1  
 4 1 CCGCTTAAAGGACTCTTACGCC 27 -13.1 -205.0 -536.1 GGTGTTAGCTGAGCTACAGAC 25 -40.2 -182.9 -471.0 641-  
 5  
 6 85B 126B 641-1B/mst A2  
 7  
 8  
 9 641-mst  
 10 1F  
 11  
 12  
 13 GAI.txt Translated Sequence  
 14  
 15 Sequence Range: 1 to 161  
 16 double strand probe 641-85B 641-FY1  
 17 CACCTCTGTC AACCG 10 20 30 40 50  
 18 AGTGACTCATGCCCTGGCCCTCTTTGGCAAGCTCTGGTGTCTAGGT  
 19 TCACATGAGTAGCGGGACCGCGAGAAACCGTTACGAGACCAAGATGCA  
 20 S V L I A L P G N A L V F Y V  
 21 TRANSLATION OF GAI.TXT [A] 641-126B  
 22 60 70 80 90 100  
 23 CCTGACCCGCAGCAAGGCCATGCGCACCGTCACCAACATCTTATCTGCT  
 24 SCACCTGGCGCTGTCGTTCCGGTACGGGTGGCAGTCGTTCTAGAAATAGACCA  
 25 V T R S K A M R T V T N I F I C  
 26 TRANSLATION OF GAI.TXT [A] 641-1B 641-BA2 641-BA (mst)  
 27 110 120 130 140 150  
 28 CCTGGCGCTCAGTGACCTGCTATCACCTCTCTGCATTCCCGTCACC  
 29 CGAACCGCGACTCCTGGACGAACTAGTGAGAGAACGTAAGGGCAGTGG  
 30 S L A B S O E F C T P V T  
 31 TRANSLATION OF GAI.TXT [A] 160  
 32 ATGAAGCCGAA  
 33 ~~ATGATCGGCTT~~  
 34 N A P X>

5 primers for 5' RACE

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DATE

CROSS REFERENCES:

# **BAYER CORPORATION**

3

**SUBJECT**

GB g3823006. by GAl.txt Aligned Sequence

Sequence Range: 1 to 481

10 20 30 40 50 60 70 80 90 100  
GB g382300 AGCGCGCAAGATGACCTCGTGTACCCGAGTGTACTCATGCCCTGGCG  
TCGCGCGTCTACTGGAGCACAGTGGCTCACATGAGTAGEGAGCGCG.

jmp1 str + 10 20  
AGTGTACTCATGCCCTGGCGC>  
GB c382300

→ AGCTTACATGCCCTGGCGC  
S V L I

60 70 80 90 100  
TCTTAGCTGTTTACAGGGTGACCAAGCAGCAAGACCAG  
AGATCGTTACGAAACTACAAATGTCACTGGTCGTCGTTCTGGTAC

GB g382300 TCTTAGCAAATGCTTGGTGTAACTGGTGACCAAGCAGCAAGACCATG  
661 - 8515

GB g382300 110 120 130 140 150 110  
CGCACCGTCACCAACATCCTTGCGCGTCAGTGACTGCTC  
GCTGGCAGTGGTGTAGATTCAGACCGAGGAACCGCGCTGGAC

jmp1 str + 6A1-120B 6A1-<sup>NST.</sup> CAGTGACCTGCTC> 12C  
GB g382300 6A1-1B TCAGTGACTGCTC

90 90. 100 110 120  
jmpl str + CGCACCCCTCACCAACATCTTATCTGCTCCTGGGGCTCAGTGA CTCGCT>  
||||| ||||| ||||| ||||| |||||  
GB 9382300 CGCACCCCTCACCAACATCTTATCTGCTCCTGGGGCTCAGTGA CTCGCT>

130 135 150 150  
impl str = ATCACCTTCTTCTGCGATTCGGCTGCGCTTACCGG

GB g382300 ATCACCTTCTTCTGCAATTCCCGTCAACATGCTCCAGAA

M K P

CATS

1000 J. Neurosci., November 1, 2006 • 26(44):9992–10003

, 541

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#### **CROSS REFERENCES:**